RAW SEQUENCE LISTING   DATE: 10/04/2000
PATENT APPLICATION: US/09/515,806   TIME: 22:32:05

Input Set : A:\38155002.app
Output Set: N:\CRF3\10042000\I515806.raw

```
69  agg ctg ttg gag gcc aag cgg aaa gaa gag cag gag caa cgt gaa atc   587
70  Arg Leu Leu Glu Ala Lys Arg Lys Glu Glu Gln Glu Gln Arg Glu Ile
71  160             165             170             175
73  ctg cat gag att cag aga agg aaa gaa gag ata aaa gaa gag aaa aaa   635
74  Leu His Glu Ile Gln Arg Arg Lys Glu Glu Ile Lys Glu Glu Lys Lys
75              180             185             190
77  agg aaa gaa atg gct aag cag gaa cgt ttg gaa att gct agt ttg tca   683
78  Arg Lys Glu Met Ala Lys Gln Glu Arg Leu Glu Ile Ala Ser Leu Ser
79              195             200             205
81  aac caa gat cat acc tct aag aag gac cca gga gga cac aga acg gct   731
82  Asn Gln Asp His Thr Ser Lys Lys Asp Pro Gly Gly His Arg Thr Ala
83          210             215             220
85  gcc att cta cat gga ggc tct cct gac ttt gta gga aat ggt aaa cat   779
86  Ala Ile Leu His Gly Gly Ser Pro Asp Phe Val Gly Asn Gly Lys His
87          225             230             235
89  cgg gca aac tcc tca gga agg tct agg cga gaa cgt cag tat tct gta   827
90  Arg Ala Asn Ser Ser Gly Arg Ser Arg Arg Glu Arg Gln Tyr Ser Val
91  240             245             250             255
93  tgt aat agt gaa gat tct cct ggc tct tgt gaa att ctg tat ttc aat   875
94  Cys Asn Ser Glu Asp Ser Pro Gly Ser Cys Glu Ile Leu Tyr Phe Asn
95              260             265             270
97  atg ggg agt cct gat cag ctc atg gtg cac aaa ggg aaa tgt att ggc   923
98  Met Gly Ser Pro Asp Gln Leu Met Val His Lys Gly Lys Cys Ile Gly
99              275             280             285
101 agt gat gaa caa ctt gga aaa tta gtc tac aat gct ttg gaa aca gcc   971
102 Ser Asp Glu Gln Leu Gly Lys Leu Val Tyr Asn Ala Leu Glu Thr Ala
103             290             295             300
105 act ggt ggc ttt gtc ttg ttg tat gag tgg gtc ctt cag tgg cag aaa   1019
106 Thr Gly Gly Phe Val Leu Leu Tyr Glu Trp Val Leu Gln Trp Gln Lys
107     305             310             315
109 aaa atg ggt cca ttc ctt acc agt caa gaa aaa gag aag att gat aag   1067
110 Lys Met Gly Pro Phe Leu Thr Ser Gln Glu Lys Glu Lys Ile Asp Lys
111 320             325             330             335
113 tgc aaa aag cag att caa gga aca gaa aca gaa ttc aac tca ctg gta   1115
114 Cys Lys Lys Gln Ile Gln Gly Thr Glu Thr Glu Phe Asn Ser Leu Val
115             340             345             350
117 aaa ttg agc cat cca aat gta gta cgc tac ctt gca atg aat ctc aaa   1163
118 Lys Leu Ser His Pro Asn Val Val Arg Tyr Leu Ala Met Asn Leu Lys
119             355             360             365
121 gag caa gac gac tcc atc gtg gtg gac att tta gtg gag cac att agt   1211
122 Glu Gln Asp Asp Ser Ile Val Val Asp Ile Leu Val Glu His Ile Ser
123             370             375             380
125 ggg gtc tct ctt gct gca cac ctg agc cac tca ggc ccc atc cct gtg   1259
126 Gly Val Ser Leu Ala Ala His Leu Ser His Ser Gly Pro Ile Pro Val
127     385             390             395
129 cat cag ctt cgc agg tac aca gct cag ctc ctg tca ggc ctt gat tat   1307
130 His Gln Leu Arg Arg Tyr Thr Ala Gln Leu Leu Ser Gly Leu Asp Tyr
131 400             405             410             415
133 ctg cac agc aat tct gtg gtg cat aag gtc ctg agt gca tct aat gtc   1355
```

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OCT 17 2000

```
134 Leu His Ser Asn Ser Val Val His Lys Val Leu Ser Ala Ser Asn Val
135                 420             425         Ser     430
137 ttg gtg gat gca gaa ggc acc gtc aag att acg gac tat agc att tct   1403
138 Leu Val Asp Ala Glu Gly Thr Val Lys Ile Thr Asp Tyr Ser Ile Ser
139             435             440                 445
141 aag cgc ctc gca gac att tgc aag gag gat gtg ttt gag caa acc cga   1451
142 Lys Arg Leu Ala Asp Ile Cys Lys Glu Asp Val Phe Glu Gln Thr Arg
143         450             455                 460
145 gtt cgt ttt agt gac aat gct ctg cct tat aaa acg ggg aag aaa gga   1499
146 Val Arg Phe Ser Asp Asn Ala Leu Pro Tyr Lys Thr Gly Lys Lys Gly
147     465             470             475
149 gat gtt tgg cgt ctt ggc ctt ctg ctg ctg tcc ctc agc caa gga cag   1547
150 Asp Val Trp Arg Leu Gly Leu Leu Leu Leu Ser Leu Ser Gln Gly Gln
151 480             485             490             495
153 gaa tgt gga gag tac cct gtg acc atc cct agt gac tta cca gct gac   1595
154 Glu Cys Gly Glu Tyr Pro Val Thr Ile Pro Ser Asp Leu Pro Ala Asp
155             500             505             510
157 ttt caa gat ttt cta aag aaa tgt gtg tgc ttg gat gac aag gaa aga   1643
158 Phe Gln Asp Phe Leu Lys Lys Cys Val Cys Leu Asp Asp Lys Glu Arg
159         515             520             525
161 tgg agt ccc cag cag ttg ttg aaa cac agc ttt ata aat ccc cag cca   1691
162 Trp Ser Pro Gln Gln Leu Leu Lys His Ser Phe Ile Asn Pro Gln Pro
163         530             535             540
165 aaa atg cct cta gtg gaa caa agt cct gaa gat tct gga gga caa gat   1739
166 Lys Met Pro Leu Val Glu Gln Ser Pro Glu Asp Ser Gly Gly Gln Asp
167     545             550             555
169 tat gtt gag act gtt att cct agc aac cgg cta ccc agt gct gcc ttc   1787
170 Tyr Val Glu Thr Val Ile Pro Ser Asn Arg Leu Pro Ser Ala Ala Phe
171 560             565             570             575
173 ttt agt gag aca cag aga cag ttt tcc cga tac ttc att gag ttt gaa   1835
174 Phe Ser Glu Thr Gln Arg Gln Phe Ser Arg Tyr Phe Ile Glu Phe Glu
175             580             585             590
177 gaa tta caa ctt ctt ggt aaa gga gct ttt gga gct gtc atc aag gtg   1883
178 Glu Leu Gln Leu Leu Gly Lys Gly Ala Phe Gly Ala Val Ile Lys Val
179             595             600             605
181 cag aac aag ttg gac ggc tgc tgc tac gca gtg aag cgc atc ccc atc   1931
182 Gln Asn Lys Leu Asp Gly Cys Cys Tyr Ala Val Lys Arg Ile Pro Ile
183         610             615             620
185 aac ccg gcc agc cgg cag ttc cgc agg atc aag ggc gaa gtg aca ctg   1979
186 Asn Pro Ala Ser Arg Gln Phe Arg Arg Ile Lys Gly Glu Val Thr Leu
187     625             630             635
189 ctg tca cgg ctg cac cat gag aac att gtg cgc tac tac aac gcc tgg   2027
190 Leu Ser Arg Leu His His Glu Asn Ile Val Arg Tyr Tyr Asn Ala Trp
191 640             645             650             655
193 atc gag cgg cac gag cgg ccg gcg gga ccg ggg acg ccg ccc ccg gac   2075
194 Ile Glu Arg His Glu Arg Pro Ala Gly Pro Gly Thr Pro Pro Pro Asp
195             660             665             670
197 tcc ggg ccc ctg gcc aag gat gac cga gct gca cgc ggg cag ccg gcg   2123
198 Ser Gly Pro Leu Ala Lys Asp Asp Arg Ala Ala Arg Gly Gln Pro Ala
```

RAW SEQUENCE LISTING   DATE: 10/04/2000
PATENT APPLICATION: US/09/515,806   TIME: 22:32:05

Input Set : A:\38155002.app
Output Set: N:\CRF3\10042000\I515806.raw

```
199            675              680              685
201 agc gac aca gac ggc ctg gac agc gta gag gcc gcc gcg ccg cca ccc   2171
202 Ser Asp Thr Asp Gly Leu Asp Ser Val Glu Ala Ala Ala Pro Pro Pro
203            690              695              700
205 atc ctc agc agc tcg gtg gag tgg agc act tcg ggc gag cgc tcg gcc   2219
206 Ile Leu Ser Ser Ser Val Glu Trp Ser Thr Ser Gly Glu Arg Ser Ala
207      705              710              715
209 agt gcc cgt ttc ccc gcc acc ggc ccg ggc tcc agc gat gac gag gac   2267
210 Ser Ala Arg Phe Pro Ala Thr Gly Pro Gly Ser Ser Asp Asp Glu Asp
211 720              725              730              735
213 gac gac gag gac gag cac ggt ggc gtc ttc tcc cag tcc ttc ctg cct   2315
214 Asp Asp Glu Asp Glu His Gly Gly Val Phe Ser Gln Ser Phe Leu Pro
215            740              745              750
217 gct tca gat tct gaa agt gat att atc ttt gac aat gaa gat gag aac   2363
218 Ala Ser Asp Ser Glu Ser Asp Ile Ile Phe Asp Asn Glu Asp Glu Asn
219            755              760              765
221 agt aaa agt cag aat cag gat gaa gat tgc aat gaa aag aat ggc tgc   2411
222 Ser Lys Ser Gln Asn Gln Asp Glu Asp Cys Asn Glu Lys Asn Gly Cys
223            770              775              780
225 cat gaa agt gag cca tca gtg acg act gag gct gtg cac tac cta tac   2459
226 His Glu Ser Glu Pro Ser Val Thr Thr Glu Ala Val His Tyr Leu Tyr
227      785              790              795
229 atc cag atg gag tac tgt gag aag agc act tta cga gac acc att gac   2507
230 Ile Gln Met Glu Tyr Cys Glu Lys Ser Thr Leu Arg Asp Thr Ile Asp
231 800              805              810              815
233 cag gga ctg tat cga gac acc gtc aga ctc tgg agg ctt ttt cga gag   2555
234 Gln Gly Leu Tyr Arg Asp Thr Val Arg Leu Trp Arg Leu Phe Arg Glu
235            820              825              830
237 att ctg gat gga tta gct tat atc cat gag aaa gga atg att cac cgg   2603
238 Ile Leu Asp Gly Leu Ala Tyr Ile His Glu Lys Gly Met Ile His Arg
239            835              840              845
241 gat ttg aag cct gtc aac att ttt ttg gat tct gat gac cat gtg aaa   2651
242 Asp Leu Lys Pro Val Asn Ile Phe Leu Asp Ser Asp Asp His Val Lys
243      850              855              860
245 ata ggt gat ttt ggt ttg gcg aca gac cat cta gcc ttt tct gct gac   2699
246 Ile Gly Asp Phe Gly Leu Ala Thr Asp His Leu Ala Phe Ser Ala Asp
247      865              870              875
249 agc aaa caa gac gat cag aca gga gac ttg att aag tca gac cct tca   2747
250 Ser Lys Gln Asp Asp Gln Thr Gly Asp Leu Ile Lys Ser Asp Pro Ser
251 880              885              890              895
253 ggt cac tta act ggg atg gtt ggc act gct ctc tat gta agc cca gag   2795
254 Gly His Leu Thr Gly Met Val Gly Thr Ala Leu Tyr Val Ser Pro Glu
255            900              905              910
257 gtc caa gga agc acc aaa tct gca tac aac cag aaa gtg gat ctc ttc   2843
258 Val Gln Gly Ser Thr Lys Ser Ala Tyr Asn Gln Lys Val Asp Leu Phe
259            915              920              925
261 agc ctg gga att atc ttc ttt gag atg tcc tat cac ccc atg gtc acg   2891
262 Ser Leu Gly Ile Ile Phe Phe Glu Met Ser Tyr His Pro Met Val Thr
263            930              935              940
```

RAW SEQUENCE LISTING   DATE: 10/04/2000
PATENT APPLICATION: US/09/515,806   TIME: 22:32:05

Input Set : A:\38155002.app
Output Set: N:\CRF3\10042000\I515806.raw

```
265 gct tca gaa agg atc ttt gtt ctc aac caa ctc aga gat ccc act tcg   2939
266 Ala Ser Glu Arg Ile Phe Val Leu Asn Gln Leu Arg Asp Pro Thr Ser
267     945                 950                 955
269 cct aag ttt cca gaa gac ttt gac gat gga gag cat gca aag cag aaa   2987
270 Pro Lys Phe Pro Glu Asp Phe Asp Asp Gly Glu His Ala Lys Gln Lys
271 960                 965                 970                 975
273 tca gtc atc tcc tgg ctg ttg aac cac gat cca gca aaa cgg ccc aca   3035
274 Ser Val Ile Ser Trp Leu Leu Asn His Asp Pro Ala Lys Arg Pro Thr
275                 980                 985                 990
277 gcc aca gaa ctg ctc aag agt gag ctg ctg ccc cca ccc cag atg gag   3083
278 Ala Thr Glu Leu Leu Lys Ser Glu Leu Leu Pro Pro Pro Gln Met Glu
279             995                 1000                1005
281 gag tca gag ctg cat gaa gtg ctg cac cac acg ctg acc aac gtg gat   3131
282 Glu Ser Glu Leu His Glu Val Leu His His Thr Leu Thr Asn Val Asp
283         1010                1015                1020
285 ggg aag gcc tac cgc acc atg atg gcc cag atc ttc tcg cag cgc atc   3179
286 Gly Lys Ala Tyr Arg Thr Met Met Ala Gln Ile Phe Ser Gln Arg Ile
287     1025                1030                1035
289 tcc cct gcc atc gat tac acc tat gac agc gac ata ctg aag ggc aac   3227
290 Ser Pro Ala Ile Asp Tyr Thr Tyr Asp Ser Asp Ile Leu Lys Gly Asn
291 1040                1045                1050                1055
293 ttc tca atc cgt aca gcc aag atg cag cag cat gtg tgt gaa acc atc   3275
294 Phe Ser Ile Arg Thr Ala Lys Met Gln Gln His Val Cys Glu Thr Ile
295                 1060                1065                1070
297 atc cgc atc ttt aaa aga cat gga gct gtt cag ttg tgt act cca cta   3323
298 Ile Arg Ile Phe Lys Arg His Gly Ala Val Gln Leu Cys Thr Pro Leu
299         1075                1080                1085
301 ctg ctt ccc cga aac aga caa ata tat gag cac aac gaa gct gcc cta   3371
302 Leu Leu Pro Arg Asn Arg Gln Ile Tyr Glu His Asn Glu Ala Ala Leu
303         1090                1095                1100
305 ttc atg gac cac agc ggg atg ctg gtg atg ctt cct ttt gac ctg cgg   3419
306 Phe Met Asp His Ser Gly Met Leu Val Met Leu Pro Phe Asp Leu Arg
307     1105                1110                1115
309 atc cct ttt gca aga tat gtg gca aga aat aat ata ttg aat tta aaa   3467
310 Ile Pro Phe Ala Arg Tyr Val Ala Arg Asn Asn Ile Leu Asn Leu Lys
311 1120                1125                1130                1135
313 cga tac tgc ata gaa cgt gtg ttc agg ccg cgc aag tta gat cga ttt   3515
314 Arg Tyr Cys Ile Glu Arg Val Phe Arg Pro Arg Lys Leu Asp Arg Phe
315                 1140                1145                1150
317 cat ccc aaa gaa ctt ctg gag tgt gca ttt gat att gtc act tct acc   3563
318 His Pro Lys Glu Leu Leu Glu Cys Ala Phe Asp Ile Val Thr Ser Thr
319         1155                1160                1165
321 acc aac agc ttt ctg ccc act gct gaa att atc tac act atc tat gaa   3611
322 Thr Asn Ser Phe Leu Pro Thr Ala Glu Ile Ile Tyr Thr Ile Tyr Glu
323         1170                1175                1180
325 atc atc caa gag ttt cca gca ctt cag gaa aga aat tac agt att tat   3659
326 Ile Ile Gln Glu Phe Pro Ala Leu Gln Glu Arg Asn Tyr Ser Ile Tyr
327     1185                1190                1195
329 ttg aac cat acc atg tta ttg aaa gca ata ctc tta cac tgt ggg atc   3707
```

FYI

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 10/04/2000
PATENT APPLICATION: US/09/515,806   TIME: 22:32:06

Input Set : A:\38155002.app
Output Set: N:\CRF3\10042000\I515806.raw

```
L:1222 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1222 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1222 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:1225 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1225 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
M:340 Repeated in SeqNo=5
L:1228 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1228 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1231 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1231 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1234 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1234 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1237 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1237 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1240 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1240 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1243 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1243 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1246 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1246 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1249 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1249 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1252 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1252 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1255 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1255 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1258 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1258 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1261 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1261 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1264 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1264 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1267 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1267 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1270 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1291 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:1291 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:1291 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:1294 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:1294 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
M:340 Repeated in SeqNo=6
```

US 095158060BP1

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Dossier: 09515806

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No.	Doccode	Number of pages
1	C.AD	1

Total number of pages: 1

Remarks:

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